

SEQUENCE LISTING

<110> Yu, Xuanchuan
Miranda, Maricar

<120> Novel Human EGF-Family Proteins and Polynucleotides Encoding the Same

<130> LEX-0317-USA

<150> US 60/275,013

<151> 2001-03-12

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3423

<212> DNA

<213> homo sapiens

<400> 1

```

atggttattt ctttgaactc atgcctgagc tttatttgtt tattgttatg ccactggatt 60
gggacagcat cacccttgaa tcttgaagac cctaattgtg gttagccactg ggaaagctac 120
tcagtgtactg tgaagagatc ataccacat cctttgtatc aaatttacta cagcagctgc 180
actgacatcc taaactgggt taaatgcacg cggcacagag tcagctatcg gacagcctat 240
cgacatgggg agaagactat gtataggcgc aagttcactg gttgtcctgg attttatgaa 300
agcggggaaa tgtgtgtccc ccaactgtgt gataaattgt tccatggctg ctgtattgtc 360
ccaaacacct gtacgtgtga gcttggctgg ggagggaaca actgctccag tgccctgcgat 420
ggtgtacact ggggtcccca ctgcaccagc cgggtccact gcaaaaatgg ggctctgtgc 480
aaccctatca cgggggcttg ccaactgtgt gcgggcttcc ggggtctggc ctgcgaggac 540
cgctgtgagc agggcaccta tggtaacgac tgtcatcaga gatgccactg ccagaatgga 600
gccacctgcg accacgtcac gggggaatgc cgctgccac caggatacac cggagccttc 660
tgtgaggatc tttgtctccc tggtaaacat ggtccacagt gtgagcagag atgcccttgt 720
caaaaatggag gagtgtgtca tcacgtcact ggagaatgct ctgccccttc tggctggatg 780
ggcacagtgt gtggtcagcc ttgccccgag ggtgcctttg gaaagaactg ttccaagaa 840
tgccagtgcc ataattggag gacgtgtgat gctgccacag gccaatgtca ttgcagtcca 900
ggatacacag gggaaacggt ccaggatgag tgtcctgttg ggacctatgg cgttctctgt 960
gctgagacct gccagtgtgt caacggaggg aagtgttacc acgtgagcg ccatgctctc 1020
tgtgaagcag gcttctgttg cgagcgctgc gaagcacgac tgtgtcctga ggggctctac 1080
ggcatcaaat gtgacaaacg gtgtccctgc caactggaaa acactcatag ctgtcaccoc 1140
ttctctggag agtgtgctg caagccgggc tggtcaggac tctactgtaa tgagacatgt 1200
tctcctgagt tctacgggga agcttgccag cagatctgca gctgccaaaa tggggcagac 1260
tgtgacagct tgactggaaa gtgcactgtg gccccaggat tcaaggaaat ggaactgctc 1320
accoccatgc ctctgggaac ctatgggata aactgttctc ctgctgttgg ctgtaaaaat 1380
gatgcagtct gctctctctg tgaactgtgc aggcaggctg gacgggggtg 1440
gactgtctca tcagatgtcc cagtggcaca tgggggcttg gctgttaact aacatgccag 1500
tgctctcaac ggggagcctg caacaccctg gacgggaact gcactgtgac acctggatgg 1560
cgcggggaga aatgcgaact tcctgccag gatggcact agcgggtgaa ctgtgtctgag 1620
cgctgcgact gcagccacgc agatggctgc caccctacca cgggcccatt ccgctgctc 1680
ccgggatgtg cagggtgtcca ctgtgacagc gtgtgtgtgt agggagcctg gggcccaaac 1740
tgctccctgc cctgctactg taaaatggg gcttcatgt ccctgatga tggcatctgc 1800
cagtggtcac caggcttccg aggcaccact tgtcagagga tctgctcccc tgggttttat 1860
gggcatctgc gcagccagac atgccacag tgcgttca caagcgggac ctgccaccac 1920
atcaccggcc tgtgtgactg ctgctctggc ttcacaggcg ccctctgcaa tgaagtgtgt 1980

```

cccagtggca gatttgggaa aaactgtgca ggaatttga cctgcaccaa caacggaacc 2040
 tgaaccccca ttgacagatc ttgtcagtgt taccgccgtt ggattggcag tgactgctct 2100
 caaccatgtc cactgtccca ctggggccca aactgcattc acacgtgcaa ctgccaat 2160
 ggagctttct cgacgccta cgatggggaa tgtaaatgca ctctggctg gacagggctc 2220
 tactgcaact agagatgtcc tctagggttt tatggaaaag attgtgcaat gatattgcaa 2280
 tgtcaaaacg gagctgact cgaccacatt tctgggcagt gtacttgcg cactggattc 2340
 gtgggagcgc actgtgagca gaagtgcctc tcaggaaacat atggctatgg ctgtgcgcag 2400
 atatgtgatt gtctgaacaa ctccacctgc gaccacatca ctgggaacct ttactgcagc 2460
 ccgggatgga agggagcgag atgtgatcaa gctgggtgta tcatagtgg aaacttgaa 2520
 agcttaagcc gaaccagtac tgcctctcct gctgattcct accagatcgg ggccattgca 2580
 ggcatcaatc ttcttgcct agttgttctc ttctactggt cattgttcat tatttata 2640
 cacaagcaga agggaaagga atcaagcatg ccagcagtta cctacacccc tgctatgagg 2700
 gtctgcaatg cagattatac catttcagga acccttctc acagcaatgg tggaaacgct 2760
 aatagccact acttccacaa tcccagttac cacacgctca cccagtgtgc cacatccct 2820
 cactgcaaca acagggacag gatgactgtc acgaagtcaa aaaacaatca actgtttgtg 2880
 aatcttaaaa atgtgaaccc tgggaagaga ggcctgtgg ggactgcac tgggacattg 2940
 ccggtctagt ggaacatcgg cggtactcct aacgagctcg gtgcttttgg acttgacaga 3000
 agctatatgg gaaaatcctt aaaagacctg ggaagaatt ctgaataaa ttcaagtaac 3060
 gtctccctaa gcagtcttga gaaccatcat gccactatta aagaccaccc tgtactatc 3120
 ccgaaaagct cagagtgtgg ttatgtggag atgaaatcgc cggcacaagg agattcccca 3180
 tatgcagaga tcaataactc aacttcagcc aacaggaaat tctatgaagt tgaacctaca 3240
 gtgagtgttg tccaaggagt attcagcaat aatgggcgtc tctccagata tccatgatgac 3300
 tctccaaaga acagtcacat ccctgtcat tatgacctgc tgcagctcag agacagttca 3360
 tctccccta agcaagagga cagtggaggt agcagcagca acacgacgag cagcagtga 3420
 tga 3473

<210> 2

<211> 1140

<212> PRT

<213> homo sapiens

<400> 2

Met Val Ile Ser Leu Asn Ser Cys Leu Ser Phe Ile Cys Leu Leu Leu
 1 5 10 15
 Cys His Trp Ile Gly Thr Ala Ser Pro Leu Asn Leu Glu Asp Pro Asn
 20 25 30
 Val Cys Ser His Trp Glu Ser Tyr Ser Val Thr Val Gln Glu Ser Tyr
 35 40 45
 Pro His Pro Phe Asp Gln Ile Tyr Tyr Thr Ser Cys Thr Asp Ile Leu
 50 55 60
 Asn Trp Phe Lys Cys Thr Arg His Arg Val Ser Tyr Arg Thr Ala Tyr
 65 70 75 80
 Arg His Gly Glu Lys Thr Met Tyr Arg Arg Lys Ser Gln Cys Cys Pro
 85 90 95
 Gly Phe Tyr Glu Ser Gly Glu Met Cys Val Pro His Cys Ala Asp Lys
 100 105 110
 Cys Val His Gly Arg Cys Ile Ala Pro Asn Thr Cys Gln Cys Glu Pro
 115 120 125
 Gly Trp Gly Gly Thr Asn Cys Ser Ser Ala Cys Asp Gly Asp His Trp
 130 135 140
 Gly Pro His Cys Thr Ser Arg Cys Gln Cys Lys Asn Gly Ala Leu Cys
 145 150 155 160
 Asn Pro Ile Thr Gly Ala Cys His Cys Ala Ala Gly Phe Arg Gly Trp
 165 170 175
 Arg Cys Glu Asp Arg Cys Glu Gln Gly Thr Tyr Gly Asn Asp Cys His
 180 185 190

Gln Arg Cys Gln Cys Gln Asn Gly Ala Thr Cys Asp His Val Thr Gly
 195 200 205
 Glu Cys Arg Cys Pro Pro Gly Tyr Thr Gly Ala Phe Cys Glu Asp Leu
 210 215 220
 Cys Pro Pro Gly Lys His Gly Pro Gln Cys Glu Gln Arg Cys Pro Cys
 225 230 235 240
 Gln Asn Gly Gly Val Cys His His Val Thr Gly Glu Cys Ser Cys Pro
 245 250 255
 Ser Gly Trp Met Gly Thr Val Cys Gly Gln Pro Cys Pro Glu Gly Arg
 260 265 270
 Phe Gly Lys Asn Cys Ser Gln Glu Cys Gln Cys His Asn Gly Gly Thr
 275 280 285
 Cys Asp Ala Ala Thr Gly Gln Cys His Cys Ser Pro Gly Tyr Thr Gly
 290 295 300
 Glu Arg Cys Gln Asp Glu Cys Pro Val Gly Thr Tyr Gly Val Leu Cys
 305 310 315 320
 Ala Glu Thr Cys Gln Cys Val Asn Gly Gly Lys Cys Tyr His Val Ser
 325 330 335
 Gly Ala Cys Leu Cys Glu Ala Gly Phe Ala Gly Glu Arg Cys Glu Ala
 340 345 350
 Arg Leu Cys Pro Glu Gly Leu Tyr Gly Ile Lys Cys Asp Lys Arg Cys
 355 360 365
 Pro Cys His Leu Glu Asn Thr His Ser Cys His Pro Met Ser Gly Glu
 370 375 380
 Cys Ala Cys Lys Pro Gly Trp Ser Gly Leu Tyr Cys Asn Glu Thr Cys
 385 390 395 400
 Ser Pro Gly Phe Tyr Gly Glu Ala Cys Gln Gln Ile Cys Ser Cys Gln
 405 410 415
 Asn Gly Ala Asp Cys Asp Ser Val Thr Gly Lys Cys Thr Cys Ala Pro
 420 425 430
 Gly Phe Lys Gly Ile Asp Cys Ser Thr Pro Cys Pro Leu Gly Thr Tyr
 435 440 445
 Gly Ile Asn Cys Ser Ser Arg Cys Gly Cys Lys Asn Asp Ala Val Cys
 450 455 460
 Ser Pro Val Asp Gly Ser Cys Thr Cys Lys Ala Gly Trp His Gly Val
 465 470 475 480
 Asp Cys Ser Ile Arg Cys Pro Ser Gly Thr Trp Gly Phe Gly Cys Asn
 485 490 495
 Leu Thr Cys Gln Cys Leu Asn Gly Gly Ala Cys Asn Thr Leu Asp Gly
 500 505 510
 Thr Cys Thr Cys Ala Pro Gly Trp Arg Gly Glu Lys Cys Glu Leu Pro
 515 520 525
 Cys Gln Asp Gly Thr Tyr Gly Leu Asn Cys Ala Glu Arg Cys Asp Cys
 530 535 540
 Ser His Ala Asp Gly Cys His Pro Thr Thr Gly His Cys Arg Cys Leu
 545 550 555 560
 Pro Gly Trp Ser Gly Val His Cys Asp Ser Val Cys Ala Glu Gly Arg
 565 570 575
 Trp Gly Pro Asn Cys Ser Leu Pro Cys Tyr Cys Lys Asn Gly Ala Ser
 580 585 590
 Cys Ser Pro Asp Asp Gly Ile Cys Glu Cys Ala Pro Gly Phe Arg Gly
 595 600 605
 Thr Thr Cys Gln Arg Ile Cys Ser Pro Gly Phe Tyr Gly His Arg Cys
 610 615 620
 Ser Gln Thr Cys Pro Gln Cys Val His Ser Ser Gly Pro Cys His His
 625 630 635 640

Ile Thr Gly Leu Cys Asp Cys Leu Pro Gly Phe Thr Gly Ala Leu Cys
 645 650 655
 Asn Glu Val Cys Pro Ser Gly Arg Phe Gly Lys Asn Cys Ala Gly Ile
 660 665 670
 Cys Thr Cys Thr Asn Asn Gly Thr Cys Asn Pro Ile Asp Arg Ser Cys
 675 680 685
 Gln Cys Tyr Pro Gly Trp Ile Gly Ser Asp Cys Ser Gln Pro Cys Pro
 690 695 700
 Pro Ala His Trp Gly Pro Asn Cys Ile His Thr Cys Asn Cys His Asn
 705 710 715 720
 Gly Ala Phe Cys Ser Ala Tyr Asp Gly Glu Cys Lys Cys Thr Pro Gly
 725 730 735
 Trp Thr Gly Leu Tyr Cys Thr Gln Arg Cys Pro Leu Gly Phe Tyr Gly
 740 745 750
 Lys Asp Cys Ala Leu Ile Cys Gln Cys Gln Asn Gly Ala Asp Cys Asp
 755 760 765
 His Ile Ser Gly Gln Cys Thr Cys Arg Thr Gly Phe Met Gly Arg His
 770 775 780
 Cys Glu Gln Lys Cys Pro Ser Gly Thr Tyr Gly Tyr Gly Cys Arg Gln
 785 790 795 800
 Ile Cys Asp Cys Leu Asn Asn Ser Thr Cys Asp His Ile Thr Gly Thr
 805 810 815
 Cys Tyr Cys Ser Pro Gly Trp Lys Gly Ala Arg Cys Asp Gln Ala Gly
 820 825 830
 Val Ile Ile Val Gly Asn Leu Asn Ser Leu Ser Arg Thr Ser Thr Ala
 835 840 845
 Leu Pro Ala Asp Ser Tyr Gln Ile Gly Ala Ile Ala Gly Ile Ile Ile
 850 855 860
 Leu Val Leu Val Val Leu Phe Leu Leu Ala Leu Phe Ile Ile Tyr Arg
 865 870 875 880
 His Lys Gln Lys Gly Lys Glu Ser Ser Met Pro Ala Val Thr Tyr Thr
 885 890 895
 Pro Ala Met Arg Val Val Asn Ala Asp Tyr Thr Ile Ser Gly Thr Leu
 900 905 910
 Pro His Ser Asn Gly Gly Asn Ala Asn Ser His Tyr Phe Thr Asn Pro
 915 920 925
 Ser Tyr His Thr Leu Thr Gln Cys Ala Thr Ser Pro His Val Asn Asn
 930 935 940
 Arg Asp Arg Met Thr Val Thr Lys Ser Lys Asn Asn Gln Leu Phe Val
 945 950 955 960
 Asn Leu Lys Asn Val Asn Pro Gly Lys Arg Gly Pro Val Gly Asp Cys
 965 970 975
 Thr Gly Thr Leu Pro Ala Asp Trp Lys His Gly Gly Tyr Leu Asn Glu
 980 985 990
 Leu Gly Ala Phe Gly Leu Asp Arg Ser Tyr Met Gly Lys Ser Leu Lys
 995 1000 1005
 Asp Leu Gly Lys Asn Ser Glu Tyr Asn Ser Ser Asn Cys Ser Leu Ser
 1010 1015 1020
 Ser Ser Glu Asn Pro Tyr Ala Thr Ile Lys Asp Pro Pro Val Leu Ile
 1025 1030 1035 1040
 Pro Lys Ser Ser Glu Cys Gly Tyr Val Glu Met Lys Ser Pro Ala Arg
 1045 1050 1055
 Arg Asp Ser Pro Tyr Ala Glu Ile Asn Asn Ser Thr Ser Ala Asn Arg
 1060 1065 1070
 Asn Val Tyr Glu Val Glu Pro Thr Val Ser Val Val Gln Gly Val Phe
 1075 1080 1085

Ser Asn Asn Gly Arg Leu Ser Gln Asp Pro Tyr Asp Leu Pro Lys Asn
 1090 1095 1100
 Ser His Ile Pro Cys His Tyr Asp Leu Leu Pro Val Arg Asp Ser Ser
 1105 1110 1115 1120
 Ser Ser Pro Lys Gln Glu Asp Ser Gly Gly Ser Ser Ser Asn Ser Ser
 1125 1130 1135
 Ser Ser Ser Glu
 1140

<210> 3
 <211> 1761
 <212> DNA
 <213> homo sapiens

<400> 3
 atggttattt ctttgaactc atgcctgagc tttatttgtt tattgttatg ccaactggatt 60
 ggcagacgat cacctctgaa tcttgaagac cctaagtgtg gttagcactg ggaagctac 120
 tcagtgaact tgcaagagtc ataccacatc ccttttgatc aaatttacta cacgagctgc 180
 actgacattc taaactgggt taaatgcacg cggcacagag tcagctatcg cagcctcat 240
 cgacatgggg agaagactat gtataggcgc aagtctcagt gttgtctctg attttatgaa 300
 agcggggaaa tgtgtgtccc ccaactgtgt gataaatgtg tccatgtctg ctgtattgt 360
 ccaaacactc gtcagtgtga gcctgggtgg ggagggacca actgtccag tgccctgcg 420
 ggtgatcact ggggtcccca ctgcaccagc cgtgtccagt gcaaaaaatg ggcctctgtgc 480
 aaccccatca ceggggcttg ccaactgtgt cggggcttcc ggggctggcg ctgcgaggac 540
 cgctgtgagc agggcaaccta tggttaacgac tgtcatcaga gatgccagt ccagaatgga 600
 gccactcgcg accacgtcac gggggaatgc cgctgccac caggatacac cggagccttc 660
 tgtgaggatc tttgtctccc tggtaaacat ggtccacagt gtgagcagag atgccctgt 720
 caaaatggag gagtgtgtca tcacgtcact ggagaatgct cttgcccttc tggctggatg 780
 ggcacagtgt gtggtcagcc ttgccccgag ggtcgctttg gaaagaactg ttcccaagaa 840
 tgccagtgcg ataattggag gacgtgtgat gctgccacag gccaatgtca ttgcagtcca 900
 ggatacacag ggggaacggt ccaggatgag tgtcctgttg ggacctatgg cgttctctgt 960
 gctgagacct gccagtgtgt caacggaggg aagtgttacc acgtgagcgg cgcattgcct 1020
 tgtgaagcag cctttgtctg cgagcgtctg gaagcacgcc tgtgtcctga ggggtctac 1080
 ggcatacaat gtgacaaaag gtgtccctgc cacttggaaa acactcatag ctgtcacccc 1140
 atgtctggag agtgtgctg caagccgggc tggtcaggac tctactgtaa tgagacatgt 1200
 tctcctggat tctacgggga agcttgcagc cagatctgca gctgccaaaa tggggcagac 1260
 tgtgacagtg tgactggaaa gtgcacctgt gccccaggat tcaaaggaat tgactgtct 1320
 accccatgcc ctctgggaac ctatgggata aactgttctc ctgctgttgg ctgtaaaaat 1380
 gatcagctgt gctctcctgt ggacgggtct gtacttgca aggcagcgtg gcacgggggt 1440
 gactgtctca tcagatgtcc cagtggcaca tggggctttg gctgttaact aacatgccag 1500
 tgcctcaacg ggggagcctg caacaccctg gacgggaact gcacgtgtgc acctggatgg 1560
 cgcggggaga aatgcgaact tccctgccag gatggcagc acgggctgaa ctgtgctgag 1620
 cgctgcgact gcagccacgc agatggctgc caccctacca cggggcattg ccgctgctc 1680
 cggggatggt cagggtgtcca ctgtgacagc gtgtgtgtg agggagcgtg gggcccaaac 1740
 tgtcctctgc cctgtactgc a

<210> 4
 <211> 586
 <212> PRT
 <213> homo sapiens

<400> 4
 Met Val Ile Ser Leu Asn Ser Cys Leu Ser Phe Ile Cys Leu Leu Leu
 1 5 10 15
 Cys His Trp Ile Gly Thr Ala Ser Pro Leu Asn Leu Glu Asp Pro Asn

465		470		475		480
Asp Cys Ser Ile Arg Cys Pro Ser Gly Thr Trp Gly Phe Gly Cys Asn						
	485		490		495	
Leu Thr Cys Gln Cys Leu Asn Gly Gly Ala Cys Asn Thr Leu Asp Gly						
	500		505		510	
Thr Cys Thr Cys Ala Pro Gly Trp Arg Gly Glu Lys Cys Glu Leu Pro						
	515		520		525	
Cys Gln Asp Gly Thr Tyr Gly Leu Asn Cys Ala Glu Arg Cys Asp Cys						
	530		535		540	
Ser His Ala Asp Gly Cys His Pro Thr Thr Gly His Cys Arg Cys Leu						
545		550		555		560
Pro Gly Trp Ser Gly Val His Cys Asp Ser Val Cys Ala Glu Gly Arg						
	565		570		575	
Trp Gly Pro Asn Cys Ser Leu Pro Cys Tyr						
	580		585			